WEST

Freeform Search

Database: US Patents Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: 119 not 116

Display: 10 Documents in Display Format: TI Starting with Number 1

Generate: ○ Hit List ◉ Hit Count ○ Image

Search | Clear | Help | Logout | Interrupt

Main Menu | Show S Numbers | Edit S Numbers | Preferences

Search History

Today's Date: 12/8/2000

DB Name	Query	Hit Count	Set Name
USPT,JPAB,EPAB,DWPI	119 not 116	22	L21 ←
USPT,JPAB,EPAB,DWPI	119 not 113	24	L20
USPT,JPAB,EPAB,DWPI	118 and 11 and 14	24	L19
USPT,JPAB,EPAB,DWPI	(18 or 19) same ((virulence adj factor$1) or toxin$1)	377	L18
USPT,JPAB,EPAB,DWPI	11 and 14	919	L17
USPT,JPAB,EPAB,DWPI	115 not 113	20	L16 ⇐
USPT,JPAB,EPAB,DWPI	14 and (16 same 19)	21	L15
USPT,JPAB,EPAB,DWPI	14 same 16 same 19	0	L14
USPT,JPAB,EPAB,DWPI	112 and database$1	50	L13 ←
USPT,JPAB,EPAB,DWPI	111 and automat$3	313	L12
USPT,JPAB,EPAB,DWPI	15 and (16 or 17 or 110)	765	L11
USPT,JPAB,EPAB,DWPI	multiplex	79121	L10
USPT,JPAB,EPAB,DWPI	DNA with (amplif$4 or amplification)	15411	L9
USPT,JPAB,EPAB,DWPI	pcr or "polymerase chain reaction"	23349	L8
USPT,JPAB,EPAB,DWPI	target with (species or microorganisms)	4342	L7
USPT,JPAB,EPAB,DWPI	array or microarray	422769	L6
USPT,JPAB,EPAB,DWPI	14 same (pathogen$1 or bacteri$2)	12231	L5
USPT,JPAB,EPAB,DWPI	food or foodborne	319342	L4
DWPI,EPAB,JPAB,USPT	(BENSON-ANDREW-K)!	0	L3 ←
DWPI,EPAB,JPAB,USPT	(BENSON-ANDREW)!	0	L2 ←
USPT,JPAB,EPAB,DWPI	((435/6)!.CCLS.)	8461	L1

09/639690

WEST

Freeform Search

Database: US Patents Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: 113 and (plurality or simultaneous)

Display: 10 Documents in Display Format: TI Starting with Number 1

Generate: ○ Hit List ◉ Hit Count ○ Image

Search | Clear | Help | Logout | Interrupt

Main Menu | Show S Numbers | Edit S Numbers | Preferences

Search History

Today's Date: 12/8/2000

DB Name	Query	Hit Count	Set Name
EPAB,DWPI	113 and (plurality or simultaneous)	3	L14
EPAB,DWPI	l3 and l6 and (nucleic adj acid$1)	97	L13
EPAB,DWPI	(l11 or l9 or l7) and @py<2000	18	L12
EPAB,DWPI	l1 and l10 and l5	9	L11
EPAB,DWPI	microorganism$1 or "micro-organism" or "micro-organisms"	42757	L10
EPAB,DWPI	l1 and l2 and l8	1	L9
EPAB,DWPI	multiplex	35347	L8
EPAB,DWPI	l1 and l2 and l5	20	L7
EPAB,DWPI	probe$1	81825	L6
EPAB,DWPI	array$1 or microarray$1	141177	L5
EPAB,DWPI	array or microarray	141173	L4
EPAB,DWPI	l1 and l2	6214	L3
EPAB,DWPI	bacteri$2 or virus$2 or pathogen$1	99990	L2
EPAB,DWPI	food or foodborne	165414	L1

WEST

Freeform Search

Database: US Patents Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: 125 and 18 and 16 and (12 or array)

Display: 10 Documents in Display Format: TI Starting with Number 1

Generate: ○ Hit List ◉ Hit Count ○ Image

Search | Clear | Help | Logout | Interrupt

Main Menu | Show S Numbers | Edit S Numbers | Preferences

Search History

Today's Date: 12/8/2000

DB Name	Query	Hit Count	Set Name
USPT,JPAB,EPAB,DWPI	l25 and l8 and l6 and (l2 or array)	3	L26
USPT,JPAB,EPAB,DWPI	(6027890 or 5824473 or 6027889 or 6001564 or 5753467 or 5795717).pn.	13	L25
USPT,JPAB,EPAB,DWPI	l23 same l6	1	L24
USPT,JPAB,EPAB,DWPI	l8 same simultaneous same detect$3	87	L23
USPT,JPAB,EPAB,DWPI	l8 same probe same array	32	L22
USPT,JPAB,EPAB,DWPI	l8 same l2	1	L21
USPT,JPAB,EPAB,DWPI	l8 same l2 same species	0	L20
USPT,JPAB,EPAB,DWPI	l14 same l2	2	L19
USPT,JPAB,EPAB,DWPI	l2 same l3 same l8	0	L18
USPT,JPAB,EPAB,DWPI	l16 not same (synthesis or sequenc$3)	6	L17
USPT,JPAB,EPAB,DWPI	l6 same l8 same (DNA with purif$7)	18	L16
USPT,JPAB,EPAB,DWPI	l6 and l8 and (DNA with purif$)	3834	L15
USPT,JPAB,EPAB,DWPI	simultaneous same species	1382	L14
USPT,JPAB,EPAB,DWPI	l4 and l2	0	L13
USPT,JPAB,EPAB,DWPI	l4 2same l2	1631	L12
USPT,JPAB,EPAB,DWPI	l4 same2 l2	1631	L11
USPT,JPAB,EPAB,DWPI	l4 same l2	0	L10
USPT,JPAB,EPAB,DWPI	l7 and l8	3	L9
USPT,JPAB,EPAB,DWPI	bacteria	143417	L8
USPT,JPAB,EPAB,DWPI	l6 same l3	14	L7
USPT,JPAB,EPAB,DWPI	automat$3	1049588	L6
USPT,JPAB,EPAB,DWPI	l3 and l4	0	L5
USPT,JPAB,EPAB,DWPI	coli same salmonella same listeria	446	L4
USPT,JPAB,EPAB,DWPI	detect$3 same l2	513	L3
USPT,JPAB,EPAB,DWPI	microarray or "probe array"	1185	L2
USPT,JPAB,EPAB,DWPI	"plurality of species"	0	L1

WEST

Freeform Search

Database: US Patents Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: 119 and enrich$4

Display: 10 Documents in Display Format: CIT Starting with Number 1

Generate: ○ Hit List ◉ Hit Count ○ Image

Search | Clear | Help | Logout | Interrupt

Main Menu | Show S Numbers | Edit S Numbers | Preferences

Search History

DB Name	Query	Hit Count	Set Name
USPT	119 and enrich$4	15	L21
USPT	118 same bacteria	2	L20
USPT	118 and bacteri$2	66	L19
USPT	116 not thuringiensis	92	L18
USPT	113 not thuringiensis	207	L17
USPT	113 not same sequenc$4	93	L16
USPT	113 same enrich$4	3	L15
USPT	113 same grow$3	11	L14
USPT	11 same 13 same (purify or purification)	217	L13
USPT	11 same (pathogen$1 or bacteri$2) same enrichment	8	L12
USPT	110 same 13	24	L11
USPT	11 same (pathogen$1 or bacteri$2) same cultur$3	275	L10
USPT	15 and (pathogen$1 or bacteri$2)	30	L9
USPT	15 same species	4	L8
USPT	15 same (pathogen$1 or bacteri$2)	0	L7
USPT	15 same food	0	L6
USPT	14 same detect$3	43	L5
USPT	11 same 12 same 13	63	L4
USPT	nucleic adj acid$1	31403	L3
USPT	microarray$1 or array$1	234593	L2
USPT	automat$3	379589	L1

Today's Date: 12/8/2000

http://westbrs:8820/bin/gate.exe?f=ffse...ovj.69.11&max=10&format=CIT&dbname=USPT

12/8/00 1:25 PM

STN search 09/639690 Dec. 08, 2000
databases searched, search terms, and selected abstracts

=> d his
(FILE 'HOME' ENTERED AT 11:39:12 ON 08 DEC 2000)

FILE 'MEDLINE, BIOSIS, AGRICOLA, CAPLUS' ENTERED AT 11:39:23 ON 08 DEC 2000

L1 916 S BENSON A?/AU
L2 813456 S FOOD OR FOODBORNE
L3 2555059 S PATHOGEN? OR MICRO-ORGANISM? OR MICROORGANISM? OR BACTERI?
L4 115825 S ARRAY? OR MICROARRAY?
L5 462876 S PROBE?
L6 237483 S AUTOMAT?
L7 77892 S DATABASE?
L8 269012 S VIRULENCE(W)FACTOR? OR TOXIN? OR VIRULENCE(W)GENE?
L9 26223 S PLURALITY OR MULTIPLEX
L10 2 S L1 AND L2 AND L3
L11 318 S L2 AND L3 AND (L4 OR L9)
L12 0 S L11 AND L6 AND L7
L13 12 S L11 AND L6
L14 2 S L11 AND L7
L15 14 S L13 OR L14
L16 24 S L11 AND L5
L17 1358 S TARGET(W)SPECIES
L18 24 S L11 AND L16
L19 0 S L11 AND L17
L20 170 S L11 AND DETECT?
L21 47 S L20 AND L8
L22 1 S L21 AND COLI AND SALMONELLA
L23 69 S L4 AND L8 AND L2
L24 37 L10 OR L15 OR L16
L25 29 DUP REM L24 (8 DUPLICATES REMOVED)

more terms after page 15

=> d ibib ab l25 1-

YOU HAVE REQUESTED DATA FROM 29 ANSWERS - CONTINUE? Y/(N):y

L25 ANSWER 1 OF 29 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:742344 CAPLUS
DOCUMENT NUMBER: 133:318245
TITLE: Amplification and separation of nucleic acid sequences using strand displacement amplification and bioelectronic microchip technology
INVENTOR(S): Nerenberg, Michael I.; Edman, Carl F.; Spargo, Catherine A.; Walker, George T.
PATENT ASSIGNEE(S): Nanogen/Becton Dickinson Partnership, USA
SOURCE: PCT Int. Appl., 137 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000062036	A1	20001019	WO 2000-US9711	20000411

W: CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRIORITY APPLN. INFO.: US 1999-290632 19990412

AB Described and disclosed are devices, methods, and compns. of matter for the **multiplex** amplification and anal. of nucleic acid sequences in a sample using novel strand displacement amplification technologies in combination with bioelectronic microchip technol. Specifically, a nucleic acid in a sample is amplified to form amplicons, the amplicons are addressed to specified electronically addressable capture sites of the bioelectronic microchip, the addressed amplicons are captured and labeled, and then the capture sites are analyzed for the presence of label. Samples may be amplified using strand displacement amplification. The invention is also amenable to other amplification methodologies well known by those skilled in the art. The capture and label steps may be by a method of universal capture with sequence-specific reporter, or by a method of sequence-specific capture with universal reporter. The label may be detected by fluorescence, chemiluminescence, electrochemiluminescence, or any other technique well known by those skilled in the art. This invention further allows for analyzing multiple nucleic acid targets on a single diagnostic platform wherein the nucleic acids may be amplified while either in direct contact with microchip components or in soln. above the microchip **array**. Thus, the described device and method was used to identify different **bacteria** on the basis of their 16S rRNA. Addnl., multiple patient samples were simultaneously analyzed for the presence of the Factor V Leiden (R506Q) gene mutation using allele-specific strand-displacement amplification (SDA) or anchored SDA. A no. of **probes** were prepd. for exonuclease-ligase strand displacement amplification and detection of numerous **bacterial** genes, e.g., gene eaeA of E. coli O157:H7.

REFERENCE COUNT: 4

REFERENCE(S): (1) Adams; US 5641658 A 1997
(2) Edman; Nucleic Acids Research 1997, V25(24), P4907
CAPLUS
(3) Heller; US 5605662 A 1997
(4) Rijks Universiteit Leiden; WO 9521938 A1 1995
CAPLUS

L25 ANSWER 7 OF 29 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2000163995 MEDLINE
DOCUMENT NUMBER: 20163995
TITLE: **Multiplex** PCR for detection and identification of lactococcal **bacteriophages**.
AUTHOR: Labrie S; Moineau S
CORPORATE SOURCE: Department of Biochemistry and Microbiology, Faculte des Sciences et de Genie, and Groupe de Recherche en Ecologie Buccale, Faculte de Medecine Dentaire, Universite Laval, Quebec, Canada G1K 7P4.
SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (2000 Mar) 66 (3) 987-94.
Journal code: 6K6. ISSN: 0099-2240.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF152410; GENBANK-AF152411; GENBANK-AF152412; GENBANK-AF152407; GENBANK-AF152409; GENBANK-AF142414; GENBANK-AF152415; GENBANK-AF152413
ENTRY MONTH: 200006
ENTRY WEEK: 20000605
AB Three genetically distinct groups of Lactococcus lactis phages are encountered in dairy plants worldwide, namely, the 936, c2, and P335 species. The **multiplex** PCR method was adapted to detect, in a single reaction, the presence of these species in whey samples or in phage lysates. Three sets of primers, one for each species, were designed based on conserved regions of their genomes. The c2-specific primers were constructed using the major capsid protein gene (mcp) as the target. The mcp sequences for three phages (eb1, Q38, and Q44) were determined and compared with the two available in the **databases**, those for phages c2 and bIL67. An 86.4% identity was found over the five mcp genes. The gene of the only major structural protein (msp) was selected as a target for the detection of 936-related phages. The msp sequences for three phages (p2, Q7, and Q11) were also established and matched with the

available data on phages sk1, bIL170, and F4-1. The comparison of the six msp genes revealed an 82. 2% identity. A high genomic diversity was observed among structural proteins of the P335-like phages suggesting that the classification of lactococcal phages within this species should be revised. Nevertheless, we have identified a common genomic region in 10 P335-like phages isolated from six countries. This region corresponded to orfF17-orf18 of phage r1t and orf20-orf21 of Tuc2009 and was sequenced for three additional P335 phages (Q30, P270, and ul40). An identity of 93.4% within a 739-bp region of the five phages was found. The detection limit of the **multiplex** PCR method in whey was 10(4) to 10(7) PFU/ml and was 10(3) to 10(5) PFU/ml with an additional phage concentration step. The method can also be used to detect phage DNA in whey powders and may also detect prophage or defective phage in the **bacterial** genome.

L25 ANSWER 8 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 2000:410198 BIOSIS
DOCUMENT NUMBER: PREV200000410198
TITLE: The use of **multiplex** PCR reactions to characterize populations of lactic acid **bacteria** associated with meat spoilage.
AUTHOR(S): Yost, C. K. (1); Nattress, F. M.
CORPORATE SOURCE: (1) Lacombe Research Centre, Agriculture and Agri-Food Canada, 6000 C and E Trail, Lacombe, Alberta, T4L 1W1 Canada
SOURCE: Letters in Applied Microbiology, (August, 2000) Vol. 31, No. 2, pp. 129-133. print.
ISSN: 0266-8254.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A rapid, systematic and reliable approach for identifying lactic acid **bacteria** associated with meat was developed, allowing for detection of Carnobacterium spp., Lactobacillus curvatus, Lact. sakei and Leuconostoc spp. Polymerase chain reaction primers specific for Carnobacterium and Leuconostoc were created from 16S rRNA oligonucleotide **probes** and used in combination with species-specific primers for the 16S/23S rRNA spacer region of Lact. curvatus and Lact. sakei in **multiplex** PCR reactions. The method was used successfully to characterize lactic acid **bacteria** isolated from a vacuum-packaged pork loin stored at 2 degreeC. Seventy isolates were selected for identification and 52 were determined to be Lact. sakei, while the remaining 18 isolates were identified as Leuconostoc spp.

L25 ANSWER 12 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1999:530386 BIOSIS
DOCUMENT NUMBER: PREV199900530386
TITLE: A **multiplex** reverse transcription polymerase chain reaction method for the detection of **foodborne** viruses.
AUTHOR(S): Rosenfield, Soraya I.; Jaykus, Lee-Ann (1)
CORPORATE SOURCE: (1) Department of Food Science, North Carolina State University, Raleigh, NC, 27695-7624 USA
SOURCE: Journal of Food Protection, (Oct., 1999) Vol. 62, No. 10, pp. 1210-1214.
ISSN: 0362-028X.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A **multiplex** reverse transcription polymerase chain reaction (RT-PCR) method was developed for the simultaneous detection of the human enteroviruses, hepatitis A virus (HAV) and Norwalk virus (NV). Poliovirus type 1 (PV1) was chosen as a model for the human enterovirus group. Three different sets of primers were used to produce three size-specific amplicons of 435 bp, 270 bp, and 192 bp for PV1, NV, and HAV, respectively. RT-PCR products were separated by agarose gel electrophoresis, and amplicon identity was confirmed by Southern transfer followed by DNA hybridization using nonradioactive, digoxigenin-labeled internal **probes**. When tested on mixed, purified virus suspensions, the **multiplex** method achieved detection limits of ltoreq1 infectious unit (PV1 and HAV) or RT-PCR-amplifiable unit (NV) for all viruses. With further streamlining efforts such as single tube amplification and liquid hybridization, **multiplex** PCR offers advantages over cell culture methodology and monoplex PCR becauseit allows for rapid and cost-effective detection of several human enteric viruses in a single reaction tube.

L25 ANSWER 13 OF 29 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:497873 CAPLUS
DOCUMENT NUMBER: 132:19267
TITLE: Semi-**automated** fluorogenic PCR assays (TaqMan) for rapid detection of Escherichia coli O157:H7 and other Shiga toxigenic E. coli
AUTHOR(S): Sharma, V. K.; Dean-Nystrom, E. A.; Casey, T. A.
CORPORATE SOURCE: Enteric Diseases and Food Safety Research Unit, National Animal Disease Center, USDA, Agricultural Research Service, Ames, IA, 50010, USA
SOURCE: Mol. Cell. Probes (1999), 13(4), 291-302
CODEN: MCPRE6; ISSN: 0890-8508
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal

LANGUAGE: English
AB Semi-**automated** detection of Enterohaemorrhagic Escherichia coli (EHEC) O157:H7 and non-O157:H7 Shiga toxin-producing E. coli (STEC) was achieved using fluorogenic polymerase chain reaction (PCR). These PCR assays were designed to amplify 80, 120 and 150 bp regions of virulence genes stx1, stx2 and eaeA, resp., using specific primers. The fluorogenic **probes** were used for specific detection of amplified products of the stx1 and stx2 genes of STEC, and the eaeA gene of EHEC O157:H7. For **multiplex** PCR assay, the three sets of primers and fluorogenic **probes** were included in one reaction to simultaneously amplify and detect any of the three targeted virulence genes. In non-**multiplex** PCR assay, each of the three virulence genes was amplified and detected in independent reactions. The specificity of these assays was evaluated using suspensions of STEC and other **bacterial** species lacking stx1 , stx2 and eaeA . The **multiplex** assay detected all STEC harboring any combination of three virulence genes. Three non-**multiplex** PCR reactions identified types of Shiga toxin genes carried by a STEC and identified STEC as either EHEC O157:H7 or non-O157:H7 STEC. Sensitivity limits of these assays in beef and feces inoculated with EHEC O157:H7 were 5.8 to 580 cfu and 1.2 to 1200 cfu, resp. These assays can be completed within 8-10 h when performed simultaneously or within 13 h if the **multiplex** assay is used as an initial screen for detecting STEC and the non-**multiplex** assay is used for subsequent detection of stx1 and stx2 of STEC and eaeA of EHEC O157:H7. (c) 1999 Academic Press.
REFERENCE COUNT: 49
REFERENCE(S): (2) Bassler, H; Applied and Environmental Microbiology 1995, V61, P3724 CAPLUS
(3) Beebakhee, G; FEMS Microbiology Letters 1992, V91, P63 CAPLUS
(4) Bilge, S; Infection and Immunity 1996, V64, P4795 CAPLUS
(7) Cebula, T; Journal of Clinical Microbiology 1995, V33, P248 CAPLUS
(9) Chen, S; Applied Environmental Microbiology 1998, V64, P4210 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L25 ANSWER 14 OF 29 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:227738 CAPLUS
DOCUMENT NUMBER: 131:40287
TITLE: Strategies for **automated** sample preparation, nucleic acid purification, and concentration of low target number nucleic acids in environmental and **food** processing samples
AUTHOR(S): Bruckner-Lea, Cynthia J.; Holman, David A.; Schuck,

Beatrice L.; Brockman, Fred J.; Chandler, Darrell P.
CORPORATE SOURCE: Pacific Northwest National Laboratory, Chemical Sensors and Microanalytical Systems, Richland, WA, 99352, USA
SOURCE: Proc. SPIE-Int. Soc. Opt. Eng. (1999), 3544(Pathogen Detection and Remediation for Safe Eating), 63-71
CODEN: PSISDG; ISSN: 0277-786X
PUBLISHER: SPIE-The International Society for Optical Engineering
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The purpose of this work is to develop a rapid, **automated** system for nucleic acid purifn. and concn. from environmental and **food** processing samples. Our current approach involves off-line filtration and cell lysis (ballistic disintegration) functions in appropriate buffers followed by **automated** nucleic acid capture and purifn. on renewable affinity matrix microcolumns. Phys. cell lysis and renewable affinity microcolumns eliminate the need for toxic org. solvents, enzyme digestions or other time-consuming sample manipulations. Within the renewable affinity microcolumn, we have examd. nucleic acid capture and purifn. efficiency with various microbead matrixes (glass, polymer, paramagnetic), surface derivatization (sequence-specific capture oligonucleotides or peptide nucleic acids), and DNA target size and concn. under variable soln. conditions and temps. Results will be presented comparing **automated** system performance relative to benchtop procedures for both clean (pure DNA from a lab. culture) and environmental (soil ext.) samples, including results which demonstrate 8 min purifn. and elution of low-copy nucleic acid targets from a crude soil ext. in a form suitable for PCR or **microarray**-based detectors. Future research will involve the development of improved affinity reagents and complete system integration, including upstream cell concn. and cell lysis functions and downstream, gene-based detectors. Results of this research will ultimately lead to improved processes and instrumentation for online, **automated** monitors for **pathogenic microorganisms** in **food**, water, air, and soil samples.
REFERENCE COUNT: 10
REFERENCE(S): (2) Chandler, D; Appl Environ Microbiol 1998, V64(2), P669 CAPLUS
(3) Chandler, D; Mol Ecol 1997, V6(5), P475 CAPLUS
(4) Fry, N; Appl Environ Microbiol 1997, V63(4), P1498 CAPLUS
(5) Holman, D; Anal Chem 1997, V69, P1763 CAPLUS
(6) Ruzicka, J; Anal Chem 1997, V69, P5024 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L25 ANSWER 15 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1998:447631 BIOSIS

DOCUMENT NUMBER: PREV199800447631
TITLE: Identification of the gene encoding the alternative sigma factor sigmaB from Listeria monocytogenes and its role in osmotolerance.
AUTHOR(S): Becker, Lynne A.; Cetin, Mehmet Sevket; Hutkins, Robert W.; **Benson, Andrew K. (1)**
CORPORATE SOURCE: (1) Dep. Food Sci. Technol., 358 Food Industry Complex, Univ. Nebraska, Lincoln, NE 68583-0919 USA
SOURCE: Journal of Bacteriology, (Sept., 1998) Vol. 180, No. 17, pp. 4547-4554.
ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Listeria monocytogenes is well known for its robust physiology, which permits growth at low temperatures under conditions of high osmolarity and low pH. Although studies have provided insight into the mechanisms used by L. monocytogenes to allay the physiological consequences of these adverse environments, little is known about how these responses are coordinated. In the studies presented here, we have cloned the sigB gene and several rsb genes from L. monocytogenes, encoding homologs of the alternative sigman factor sigmaB and the RsbUVWX proteins, which govern transcription of a general stress regulon in the related **bacterium** Bacillus subtilis. The L. monocytogenes and B. subtilis sigB and rsb genes are similar in sequence and physical organization; however, we observed that the activity of sigmaB in L. moocytogenes was uniquely responsive to osmotic upshifting, temperature downshifting, and the presence of EDTA in the growth medium. The magnitude of the response was greatest after an osmotic upshift, suggesting a role for sigmaB in coordinating osmotic responses in L. monocytogenes. A null mutation in the sigB gene led to substantial defects in the ability of L. monocytogenes to use betaine and carnitine as osmoprotectants. Subsequent measurements of betaine transport confirmed that the absence of sigmaB reduced the ability of the cells to accumulate betaine. Thus, sigmaB coordinates responses to a variety of physical and chemical signals, and its function facilitates the growth of L. monocytogenes under conditions of high osmotic strength.

L25 ANSWER 16 OF 29 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:524875 CAPLUS
TITLE: Microbial monitoring using hybridization assays and artificial RNA labels.
AUTHOR(S): Walia, R. P.; Murphy, J. C.; Fox, G. E.; Willson, R. C.
CORPORATE SOURCE: Dept Chem Eng, U H, Houston, TX, 77204, USA
SOURCE: Book of Abstracts, 216th ACS National Meeting, Boston, August 23-27 (1998), BIOT-223. American Chemical Society: Washington, D. C.

CODEN: 66KYA2
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB Measurement of the nos. and distribution of **microorganisms** is essential to an understanding of bioremediation, **food** contamination and microbial **pathogenesis**. Mol. anal. of recalcitrant populations has been revolutionized by rRNA hybridization-based assays, esp. DNA **probe arrays** ("DNA chips"). The application of these methods to complex environmental samples requires the extn. of nucleic acids in sufficient purity for anal. We have devised a non-perturbing microbial labeling technique employing Stable Artificial RNAs (SAR's), engineered rRNA analogs which display unique identifier sequences and are compatible with DNA chip detection. Many applications of these technologies require development of convenient extn. methods suitable for on-site or field analyses. By exploting the chem. differences between rRNA and contaminating species such as humic acids, DNA and proteins, we are developing methods of isolating highly pure nucleic acid samples for hybridization anal.

L25 ANSWER 17 OF 29 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:579861 CAPLUS
DOCUMENT NUMBER: 127:215947
TITLE: Detection of nucleic acid sequence differences using the ligase detection reaction with addressable **array**
INVENTOR(S): Barany, Francis; Barany, George; Hammer, Robert P.; Kempe, Maria; Blok, Herman; Zirvi, Monib
PATENT ASSIGNEE(S): Cornell Research Foundation, Inc., USA; University of Minnesota; Louisiana State University; Barany, Francis; Barany, George; Hammer, Robert P.; Kempe, Maria; Blok, Herman; Zirvi, Monib
SOURCE: PCT Int. Appl., 124 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9731256	A2	19970828	WO 1997-US1535	19970205
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2244891	AA	19970828	CA 1997-2244891	19970205
AU 9727997	A1	19970910	AU 1997-27997	19970205
EP 920440	A2	19990609	EP 1997-922283	19970205
R: CH, DE, FR, GB, IT, LI, SE				
PRIORITY APPLN. INFO.:			US 1996-11359	19960209
			WO 1997-US1535	19970205

AB The present invention describes a method for identifying one or more of a **plurality** of sequences differing by one or more single base changes, insertions, deletions, or translocations in a **plurality** of target nucleotide sequences. The method includes a ligation phase, a capture phase, and a detection phase. The ligation phase utilizes a ligation detection reaction between one oligonucleotide **probe**, which has a target sequence-specific portion and an addressable **array**-specific portion, and a second oligonucleotide **probe** , having a target sequence-specific portion and a detectable label. After the ligation phase, the capture phase is carried out by hybridizing the ligated oligonucleotide **probes** to a solid support with an **array** of immobilized capture oligonucleotides at least some of which are complementary to the addressable **array**-specific portion. Following completion of the capture phase, a detection phase is carried out to detect the labels of ligated oligonucleotide **probes** hybridized to the solid support. The ligation phase can be preceded by an amplification process. The present invention also relates to a kit for practicing this method, a method of forming **arrays** on solid supports, and the supports themselves.

L25 ANSWER 18 OF 29 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 97192330 MEDLINE
DOCUMENT NUMBER: 97192330
TITLE: Molecular diagnostics for dairy-borne **pathogens**.
AUTHOR: Batt C A
CORPORATE SOURCE: Department of Food Science, Cornell University, Ithaca, NY 14853, USA.
SOURCE: JOURNAL OF DAIRY SCIENCE, (1997 Jan) 80 (1) 220-9. Ref: 39
Journal code: HWV. ISSN: 0022-0302.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199706
ENTRY WEEK: 19970604

AB Advances in diagnostic assays based on nucleic acids will revolutionize the ability of the industry to maintain the safety of dairy **foods** . Two complementary assay formats are explored, one of which permits the rapid detection of **bacterial pathogens** and the other the identification of reservoirs of these **pathogens**. The first format is an assay based on the polymerase chain reaction that employs homogeneous detection (TaqMan polymerase chain reaction detection; Perkin Elmer, Applied Biosystems Division, Foster City, CA) of the target sequence. This assay has been applied to the detection of Listeria monocytogenes. A primary problem with current assays that are based on polymerase chain reaction is the complexity of sample handling and the quantification of the initial target number. This fluorogenic assay takes advantage of the endogenous 5',3'-endonuclease activity in Taq DNA polymerase. Approximately 100 samples can be analyzed in 2 to 3 h with a sensitivity of < 50 cells and a dynamic range of > 1000-fold. The TaqMan polymerase chain reaction detection assay is a robust format that is readily applicable to a wide **array** of other **pathogens** found in **foods** and in the environment. The second format is an instrument for **automated** ribosomal RNA analysis (Riboprinter; DuPont, Wilmington, DE) that can be used to locate the reservoirs harboring the **bacterial pathogen**. Use of this typing method it has been shown that, although a number of different ribotypes can be isolated from a single environmental sample, only a selected number of these strains apparently have the ability to cause disease. The future of **food** microbiology lies in the development and integration of molecular methods that can be **automated** into a testing regimen that extends from the farm to finished products.

L25 ANSWER 19 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS DUPLICATE 3
ACCESSION NUMBER: 1996:363525 BIOSIS
DOCUMENT NUMBER: PREV199699085881
TITLE: A **multiplex** PCR for rapid identification of Shiga-like toxin-producing Escherichia coli O157:H7 isolated from **foods**.
AUTHOR(S): Deng, Ming Y.; Fratamico, Pina M. (1)
CORPORATE SOURCE: (1) Microbial Food Safety Res. Unit, U.S. Dep. Agric., Eastern Regional Res. Cent., Agric. Res. Service, 600 East Mermaid Lane, Wyndmoor, PA 19038 USA
SOURCE: Journal of Food Protection, (1996) Vol. 59, No. 6, pp. 570-576.
ISSN: 0362-028X.
DOCUMENT TYPE: Article
LANGUAGE: English
AB For rapid and specific identification of enterohemorrhagic Escherichia coli (EHEC) serotype O157:H7 isolated from **food** samples, experimental conditions for a **multiplex** polymerase chain

reaction (PCR) were optimized and a multiple digoxigenin (DIG)labeled oligonucleotide **probe** hybridization (DLOPH) assay was developed. A suspect colony from MacConkey sorbitol agar containing 5-bromo-4-chloro-3-indoxyl-beta-D-glucuronide (MSABCIG) was used for the **multiplex** PCR. Three different DNA sequences of E. coli O157:H7 were amplified simultaneously in the PCR: a specific fragment of an attaching and effacing gene (eae gene), conserved sequences of Shiga-like toxins (SLT) I and II, and a fragment of the 60-MDa plasmid. The identities of PCR products were confirmed by hybridization using DIG-labeled internal oligonucleotide **probes** and colorimetric detection with anti-DIG Fab fragments conjugated to alkaline phosphatase. This method yielded positive results with all reference strains of EHEC serogroup O157, including serotypes O157:H7, O157:NM, and O157:H-, and negative results were obtained with all strains of nontoxigenic E. coli serogroup O157, other serotypes of E. coli, and other **bacterial** species. The detection limit of the method was 65 colony-forming units (CFU) of E. coli O157:H7. All 29 cultures of EHEC O157:H7 isolated from meat samples and identified by biochemical and serological tests were positive in the **multiplex** PCR. EHEC O157:H7 was identified from all of 70 experimentally inoculated ground beef and milk samples which had initial inocula of 4 to 9 CFU/g (ml) and were subjected to a 6-h enrichment culturing. The **multiplex** PCR procedure could be very useful for routine examinations of **food** samples for the presence of EHEC O157.

L25 ANSWER 21 OF 29 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:35735 CAPLUS
DOCUMENT NUMBER: 126:115285
TITLE: Ultrathin oligonucleotide layers for fluorescence based DNA-sensors
AUTHOR(S): Furch, M.; Ueberfeld, J.; Hartmann, A.; Bock, D.; Seeger, S.
CORPORATE SOURCE: Physikalisch-Chemisches Inst., Univ. Heidelberg, Heidelberg, 69120, Germany
SOURCE: Proc. SPIE-Int. Soc. Opt. Eng. (1996), 2928(Biomedical Systems and Technologies), 220-226
CODEN: PSISDG; ISSN: 0277-786X
PUBLISHER: SPIE-The International Society for Optical Engineering
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Preliminary investigations into the design of an affinity sensor using evanescent wave technol. conc. upon the means of immobilization of the receptor mols. In this work DNA served as the selective recognition element. The mol. principle of a sequence-selective biosensor for DNA is

based on a sandwich-hybridization assay wherein the analyte, a single-stranded (ss)DNA, bound specifically to both an immobilized capture **probe** and a dye-labeled oligonucleotide in free soln. The efficiency of the capture **array** depends on the d. of highly organized oligonucleotides on the waveguide surface and correlates therefore directly with the specificity and the sensitivity of the sensor. In the present approach using the Langmuir-Blodgett technique cinnamoylbutylether-cellulose monolayers were transferred onto optical fibers or planar waveguides. These films served as matrixes for the immobilization of biotinylated oligonucleotides via streptavidin. For the first time streptavidin was immobilized by that manner. The specificity of the streptavidin layer or the following bounded nucleic acid mols. were controlled by an ELISA. Finally, this application has also shown to be suitable for the detection of Salmonella, which is an important **pathogen** assocd. with acute gastroenteritidis and **food** borne diseases.

L25 ANSWER 22 OF 29 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1995:781986 CAPLUS
DOCUMENT NUMBER: 123:220262
TITLE: A method for identifying **microorganisms** based on nucleic acid amplification and gel electrophoresis
INVENTOR(S): Fluit, Adriaan Camille; Widjojoatmodjo, Myra Noorely
PATENT ASSIGNEE(S): U-Gene Research B.V., Neth.
SOURCE: PCT Int. Appl., 34 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9513396	A2	19950518	WO 1994-NL283	19941111
WO 9513396	A3	19950608		
W: CA, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
NL 9301957	A	19950601	NL 1993-1957	19931111

PRIORITY APPLN. INFO.: NL 1993-1957 19931111
AB A method is provided for the identification of a **microorganism**, in particular a **bacterium**, present in a sample. Nucleic acid (DNA or RNA) of the **microorganism** present in the sample is subjected to PCR or a different nucleic acid amplification method, utilizing one or more sets of universal primers based on a gene of the **microorganism** to be identified which comprises both conserved and

variable regions (in particular the 16 S rRNA gene), the primers being chosen in conserved areas which enclose a variable region. The product of the amplification is brought into single-stranded form, if necessary, and subjected to electrophoresis by which single-stranded nucleic acids of equal lengths can be sepd. from each other on the basis of differences in nucleotide sequence. The electrophoresed nucleic acid is detected and its position compared with those of a set of ref. nucleic acids of known **microorganisms**. Set of suitable aids for practicing the method are provided. Thus, when a PCR primer pair based on regions 103-119 and 341-347 of the 16 S rRNA gene is applied to 114 **bacterial** strains selected from 40 species and 15 genera, the 35 different single-stranded DNA band patterns that result are species-specific. **Multiplex** PCR with a second primer set allowed addnl. discrimination. SSDM (sequence-dependent differences in mobility)-PCR using fluorescein isothiocyanate-labeled primers followed by anal. on an **automatic** sequencer also yielded species-dependent patterns.

L25 ANSWER 23 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1994:332233 BIOSIS
DOCUMENT NUMBER: PREV199497345233
TITLE: **Multiplex** PCR DNA amplification and gene **probe** methods for species-specific simultaneous detection of enteropathogenic/toxigenic, enterohemorrhagic, and enteroinvasive Escherichia coli in artificially contaminated ground beef.
AUTHOR(S): Lett, P.; Jones, D. D.; Bej, A. K.
CORPORATE SOURCE: Dep. Biol., Univ. Ala. at Birmingham, AL 35294-1170 USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (1994) Vol. 94, No. 0, pp. 386.
Meeting Info.: 94th General Meeting of the American Society for Microbiology Las Vegas, Nevada, USA May 23-27, 1994
ISSN: 1060-2011.
DOCUMENT TYPE: Conference
LANGUAGE: English

L25 ANSWER 24 OF 29 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1993:377181 BIOSIS
DOCUMENT NUMBER: PREV199345048606
TITLE: Detection of Salmonella spp., Vibrio cholerae, and Vibrio vulnificus from artificially contaminated shellfish by **multiplex** polymerase chain reactions (PCR) and gene **probes**.
AUTHOR(S): Bej, A. K.; Jones, D. D.
CORPORATE SOURCE: Univ. Alabama Birmingham, Birmingham, AL 35294-1170 USA
SOURCE: Abstracts of the General Meeting of the American Society

for Microbiology, (1993) Vol. 93, No. 0, pp. 384.
Meeting Info.: 93rd General Meeting of the American Society for Microbiology Atlanta, Georgia, USA May 16-20, 1993
ISSN: 1060-2011.
DOCUMENT TYPE: Article
LANGUAGE: English

L25 ANSWER 25 OF 29 MEDLINE
ACCESSION NUMBER: 93119133 MEDLINE
DOCUMENT NUMBER: 93119133
TITLE: Rapid and sensitive method for detection of Shiga-like toxin-producing Escherichia coli in ground beef using the polymerase chain reaction.
AUTHOR: Gannon V P; King R K; Kim J Y; Thomas E J
CORPORATE SOURCE: Animal Diseases Research Institute, Agriculture Canada, Lethbridge, Alberta..
SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (1992 Dec) 58 (12) 3809-15.
Journal code: 6K6. ISSN: 0099-2240.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199304
AB A rapid and sensitive method for detection of Shiga-like toxin (SLT)-producing Escherichia coli (SLT-EC) with the polymerase chain reaction (PCR) is described. Two pairs of oligonucleotide primers homologous to SLTI and SLTII genes, respectively, were used in **multiplex** PCR assays. The first pair generated a ca. 600-bp PCR product with DNA from all SLTI-producing E. coli tested but not from E. coli strains that produce SLTII or variants of SLTII. The second pair generated a ca. 800-bp PCR product with DNA from E. coli strains that produce SLTII or variants of SLTII but not from SLTI-producing E. coli. When used in combination, the SLTI and SLTII oligonucleotide primers amplified DNA from all of the SLT-EC tested. No PCR products were obtained with SLT primers with DNA from 28 E. coli strains that do not produce SLT or 44 strains of 28 other **bacterial** species. When ground beef samples were inoculated with SLT-EC strains 319 (O157:H7; SLTI and SLTII), H30 (O26:H11; SLTI), and B2F1/3 (O91:H21; SLTII variants VT2ha and VT2hb) and cultured in modified Trypticase soy broth for 6 h at 42 degrees C, an initial sample inoculum of as few as 1 CFU of these SLT-EC strains per g could be detected in PCR assays with DNA extracted from the broth cultures.

STN more searching 09/639390 Dec. 11, 2000
databases searched, search terms, selected abstracts

=> d his
(FILE 'HOME' ENTERED AT 15:35:26 ON 11 DEC 2000)

FILE 'MEDLINE, BIOSIS, AGRICOLA, CAPLUS' ENTERED AT 15:35:34 ON 11 DEC 2000
L1 813524 S FOOD OR FOODBORNE
L2 115854 S ARRAY? OR MICROARRAY?
L3 1873 S L1 AND L2
L4 1619592 S SPECIES
L5 245 S L1 AND L2 AND L3 AND L4
L6 237507 S AUTOMAT?
L7 77911 S DATABASE?
L8 2 S L5 AND L6
L9 1844375 S OLIGONUCLEOTIDE? OR DNA OR NUCLEIC(W)ACID?
L10 117206 S RIBOSOMAL
L11 13283 S L2 AND (L9 OR L10)
L12 70 S L11 AND L1
L13 52 DUP REM L12 (18 DUPLICATES REMOVED)
L14 37 S L13 AND PY<2000

=> d ibib ab l14 1-

YOU HAVE REQUESTED DATA FROM 37 ANSWERS - CONTINUE? Y/(N):y

L14 ANSWER 1 OF 37 MEDLINE
ACCESSION NUMBER: 2000126777 MEDLINE
DOCUMENT NUMBER: 20126777
TITLE: Future trends in diagnosis using laboratory-on-a-chip technologies.
AUTHOR: Talary M S; Burt J P; Pethig R
CORPORATE SOURCE: Institute of Molecular and Biomolecular Electronics, University of Wales, Bangor, U.K.
SOURCE: PARASITOLOGY, **(1998)** 117 Suppl S191-203. Ref: 11
Journal code: OR0. ISSN: 0031-1820.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005

ENTRY WEEK: 20000501
AB There has been an enormous growth in the development of biotechnological applications, where advances in the techniques of microelectronic fabrication and the technologies of miniaturization and integration in semiconductor industries are being applied to the production of Laboratory-on-a-Chip devices. The aim of this development is to create devices that will perform the same processes that are currently carried out in the laboratory in reduced timescales, at a lower cost, requiring less reagents, and with a greater resolution of detection and specificity. The expectations of this Laboratory-on-a-Chip revolution is that this technology will facilitate rapid advances in gene discovery, genetic mapping and gene expression with broader applications ranging from infectious diseases and cancer diagnostics to **food** quality and environmental testing. A review of the current state of development in this field reveals the scale of the ongoing revolution and serves to highlight the advances that can be perceived in the development of Laboratory-on-a-Chip technologies. Since miniaturization can be applied to such a wide range of laboratory processes, some of the sub-units that can be used as building blocks in these devices are described, with a brief description of some of the fabrication processes that can be used to create them.

L14 ANSWER 2 OF 37 MEDLINE
ACCESSION NUMBER: 2000000190 MEDLINE
DOCUMENT NUMBER: 20000190
TITLE: **DNA-microarrays and food** -biotechnology.
AUTHOR: Kuipers O P; de Jong A; Holsappel S; Bron S; Kok J; Hamoen L W
CORPORATE SOURCE: Department of Genetics, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Haren, The Netherlands.. o.p.kuipers@biol.rug.nl
SOURCE: ANTONIE VAN LEEUWENHOEK, **(1999 Jul-Nov)** 76 (1-4) 353-5.
Journal code: 6JE. ISSN: 0003-6072.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200001
ENTRY WEEK: 20000104

L14 ANSWER 3 OF 37 MEDLINE
ACCESSION NUMBER: 1999439582 MEDLINE
DOCUMENT NUMBER: 99439582

TITLE: Genomics for **food** biotechnology: prospects of the use of high-throughput technologies for the improvement of **food** microorganisms.
AUTHOR: Kuipers O P
CORPORATE SOURCE: Department of Genetics Groningen Biomolecular Sciences and Biotechnology Institute University of Groningen PO Box 14, 9750 AA, Haren, The Netherlands.. o.p.kuipers@biol.rug.nl
SOURCE: CURRENT OPINION IN BIOTECHNOLOGY, **(1999 Oct)** 10 (5) 511-6. Ref: 45
Journal code: A92. ISSN: 0958-1669.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY WEEK: 20000204
AB Functional genomics is currently the most effective approach for increasing the knowledge at the molecular level of metabolic and adaptive processes in whole cells. High-throughput technologies, such as **DNA microarrays**, and improved two-dimensional electrophoresis methods combined with tandem mass-spectroscopy, supported by bioinformatics, are useful tools for **food** biotechnology, which depends on detailed knowledge of the properties of **food** microbes (and pathogens) in their industrial, **food** and consumer environments. Genomics of **food** microbes, based on rapidly emerging genome sequence information, generates valuable knowledge that can be used for metabolic engineering, improving cell factories and development of novel preservation methods. Furthermore, pre- and probiotic studies, characterization of stress responses, studies of microbial ecology and, last but not least, development of novel risk assessment procedures will be facilitated.

L14 ANSWER 4 OF 37 MEDLINE
ACCESSION NUMBER: 1999147213 MEDLINE
DOCUMENT NUMBER: 99147213
TITLE: Chemoselective biosensors.
AUTHOR: Lowe C R
CORPORATE SOURCE: Institute of Biotechnology, University of Cambridge, Tennis Court Road, Cambridge CB2 1QT, UK.. crl1@biotech.cam.ac.uk
SOURCE: CURRENT OPINION IN CHEMICAL BIOLOGY, **(1999 Feb)** 3 (1) 106-11. Ref: 60
Journal code: C4U. ISSN: 1367-5931.
PUB. COUNTRY: ENGLAND: United Kingdom

Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY WEEK: 19990604
AB New opportunities for biosensors are now appearing in clinical and genetic diagnostics, genomics, environmental protection, **food** processing and safety, drug discovery and bioprocess monitoring. Concerns about the cost, stability and selectivity of previous sensor technologies are being addressed by developing new recognition systems and their integration into transducers, micro- and nanofabricated devices, **array** technologies and novel magnetic, acoustic and optical transduction systems.

L14 ANSWER 6 OF 37 MEDLINE
ACCESSION NUMBER: 97192330 MEDLINE
DOCUMENT NUMBER: 97192330
TITLE: Molecular diagnostics for dairy-borne pathogens.
AUTHOR: Batt C A
CORPORATE SOURCE: Department of Food Science, Cornell University, Ithaca, NY 14853, USA.
SOURCE: JOURNAL OF DAIRY SCIENCE, **(1997 Jan)** 80 (1) 220-9. Ref: 39
Journal code: HWV. ISSN: 0022-0302.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199706
ENTRY WEEK: 19970604
AB Advances in diagnostic assays based on **nucleic acids** will revolutionize the ability of the industry to maintain the safety of dairy **foods**. Two complementary assay formats are explored, one of which permits the rapid detection of bacterial pathogens and the other the identification of reservoirs of these pathogens. The first format is an assay based on the polymerase chain reaction that employs homogeneous detection (TaqMan polymerase chain reaction detection; Perkin Elmer, Applied Biosystems Division, Foster City, CA) of the target sequence. This assay has been applied to the detection of Listeria monocytogenes. A primary problem with current assays that are based on polymerase chain reaction is the complexity of sample handling and the quantification of

the initial target number. This fluorogenic assay takes advantage of the endogenous 5',3'-endonuclease activity in Taq **DNA** polymerase. Approximately 100 samples can be analyzed in 2 to 3 h with a sensitivity of < 50 cells and a dynamic range of > 1000-fold. The TaqMan polymerase chain reaction detection assay is a robust format that is readily applicable to a wide **array** of other pathogens found in **foods** and in the environment. The second format is an instrument for automated **ribosomal** RNA analysis (Riboprinter; DuPont, Wilmington, DE) that can be used to locate the reservoirs harboring the bacterial pathogen. Use of this typing method it has been shown that, although a number of different ribotypes can be isolated from a single environmental sample, only a selected number of these strains apparently have the ability to cause disease. The future of **food** microbiology lies in the development and integration of molecular methods that can be automated into a testing regimen that extends from the farm to finished products.

L14 ANSWER 18 OF 37 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1990:131035 BIOSIS
DOCUMENT NUMBER: BA89:69846
TITLE: SCREENING **DNA** PROBES USING THE HYDROPHOBIC GRID-MEMBRANE FILTER.
AUTHOR(S): PETERKIN P I; IDZIAK E S; SHARPE A N
CORPORATE SOURCE: BUREAU MICROBIAL HAZARDS, HEALTH PROTECTION BRANCH HEALTH AND WELFARE CAN., TUNNEY'S PASTURE, OTTAWA, CAN. K1A 0L2.
SOURCE: FOOD MICROBIOL (LOND), (1989) 6 (4), 281-284. CODEN: FOMIE5. ISSN: 0740-0020.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Seven clones showing .beta.-hemolysis, from a Listeria monocytogenes genomic library, were assessed by a hydrophobic grid-membrane filter (HGMF) screening technique for their specificity as **DNA** probes. Plasmid **DNA** from each of the clones was screened by colony hybridization against replicates of a library of 100 organisms, consisting of 70 L. monocytogenes strains, ten other Listeria spp., and 20 organisms of other genera, **arrayed** on an HGMF. Clones showing potential for use in analytical **food** microbiology were identified by this means.

L14 ANSWER 21 OF 37 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:227738 CAPLUS
DOCUMENT NUMBER: 131:40287
TITLE: Strategies for automated sample preparation, **nucleic acid** purification, and concentration of low target number **nucleic acids** in environmental and **food** processing samples
AUTHOR(S): Bruckner-Lea, Cynthia J.; Holman, David A.; Schuck, Beatrice L.; Brockman, Fred J.; Chandler, Darrell P.
CORPORATE SOURCE: Pacific Northwest National Laboratory, Chemical Sensors and Microanalytical Systems, Richland, WA, 99352, USA
SOURCE: Proc. SPIE-Int. Soc. Opt. Eng. (**1999**), 3544(Pathogen Detection and Remediation for Safe Eating), 63-71
CODEN: PSISDG; ISSN: 0277-786X
PUBLISHER: SPIE-The International Society for Optical Engineering
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The purpose of this work is to develop a rapid, automated system for **nucleic acid** purifn. and concn. from environmental and **food** processing samples. Our current approach involves off-line filtration and cell lysis (ballistic disintegration) functions in appropriate buffers followed by automated **nucleic acid** capture and purifn. on renewable affinity matrix microcolumns. Phys. cell lysis and renewable affinity microcolumns eliminate the need for toxic org. solvents, enzyme digestions or other time-consuming sample manipulations. Within the renewable affinity microcolumn, we have examd. **nucleic acid** capture and purifn. efficiency with various microbead matrixes (glass, polymer, paramagnetic), surface derivatization (sequence-specific capture **oligonucleotides** or peptide **nucleic acids**), and **DNA** target size and concn. under variable soln. conditions and temps. Results will be presented comparing automated system performance relative to benchtop procedures for both clean (pure **DNA** from a lab. culture) and environmental (soil ext.) samples, including results which demonstrate 8 min purifn. and elution of low-copy **nucleic acid** targets from a crude soil ext. in a form suitable for PCR or **microarray**-based detectors. Future research will involve the development of improved affinity reagents and complete system integration, including upstream cell concn. and cell lysis functions and downstream, gene-based detectors. Results of this research will ultimately lead to improved processes and instrumentation for online, automated monitors for pathogenic microorganisms in **food**, water, air, and soil samples.
REFERENCE COUNT: 10
REFERENCE(S): (2) Chandler, D; Appl Environ Microbiol 1998, V64(2), P669 CAPLUS
(3) Chandler, D; Mol Ecol 1997, V6(5), P475 CAPLUS
(4) Fry, N; Appl Environ Microbiol 1997, V63(4), P1498

CAPLUS
(5) Holman, D; Anal Chem 1997, V69, P1763 CAPLUS
(6) Ruzicka, J; Anal Chem 1997, V69, P5024 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 24 OF 37 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:524875 CAPLUS
TITLE: Microbial monitoring using hybridization assays and artificial RNA labels.
AUTHOR(S): Walia, R. P.; Murphy, J. C.; Fox, G. E.; Willson, R. C.
CORPORATE SOURCE: Dept Chem Eng, U H, Houston, TX, 77204, USA
SOURCE: Book of Abstracts, 216th ACS National Meeting, Boston, August 23-27 (**1998**), BIOT-223. American Chemical Society: Washington, D. C.
CODEN: 66KYA2
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB Measurement of the nos. and distribution of microorganisms is essential to an understanding of bioremediation, **food** contamination and microbial pathogenesis. Mol. anal. of recalcitrant populations has been revolutionized by rRNA hybridization-based assays, esp. **DNA** probe **arrays** ("**DNA** chips"). The application of these methods to complex environmental samples requires the extn. of **nucleic acids** in sufficient purity for anal. We have devised a non-perturbing microbial labeling technique employing Stable Artificial RNAs (SAR's), engineered rRNA analogs which display unique identifier sequences and are compatible with **DNA** chip detection. Many applications of these technologies require development of convenient extn. methods suitable for on-site or field analyses. By exploting the chem. differences between rRNA and contaminating species such as humic acids, **DNA** and proteins, we are developing methods of isolating highly pure **nucleic acid** samples for hybridization anal.

L14 ANSWER 25 OF 37 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:42541 CAPLUS
DOCUMENT NUMBER: 128:72663
TITLE: Broad specificity affinity **arrays**: a qualitative approach to complex sample discrimination
INVENTOR(S): Mecklenburg, Michael; Danielsson, Bengt; Winquist, Fredrik
PATENT ASSIGNEE(S): Interactiva Biotechnologie G.m.b.H., Germany; Mecklenburg, Michael; Danielsson, Bengt; Winquist, Fredrik

SOURCE: PCT Int. Appl., 29 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9749989	A2	19971231	WO 1997-EP3317	19970624 <--
W: AU, CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
SE 9602545	A	19971226	SE 1996-2545	19960625 <--
CA 2258941	AA	19971231	CA 1997-2258941	19970624 <--
AU 9734363	A1	19980114	AU 1997-34363	19970624 <--
EP 1021713	A2	20000726	EP 1997-930394	19970624
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2000513436	T2	20001010	JP 1997-543108	19970624

PRIORITY APPLN. INFO.: SE 1996-2545 19960625
WO 1997-EP3317 19970624

AB Described is a method for discriminating complex biol. samples using an **array** of discrete biol. sensing elements immobilized onto a solid support in which constituents bound to the sensor **array** are directly detd. by measuring the mass increase on the surface; data anal. of said method is performed using neutral network or statical based pattern recognition techniques. In a preferred embodiment the liq. sample is tested for the presence of sol. constituent(s) by contacting said sample with said sensor **array** under specific conditions, removing unbound sample constituent(s), detg. the mass increase on the surface and comparing said mass increase data with a ref. std. using pattern recognition software.

L14 ANSWER 26 OF 37 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:579861 CAPLUS
DOCUMENT NUMBER: 127:215947
TITLE: Detection of **nucleic acid** sequence differences using the ligase detection reaction with addressable **array**
INVENTOR(S): Barany, Francis; Barany, George; Hammer, Robert P.; Kempe, Maria; Blok, Herman; Zirvi, Monib
PATENT ASSIGNEE(S): Cornell Research Foundation, Inc., USA; University of Minnesota; Louisiana State University; Barany, Francis; Barany, George; Hammer, Robert P.; Kempe, Maria; Blok, Herman; Zirvi, Monib
SOURCE: PCT Int. Appl., 124 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9731256	A2	19970828	WO 1997-US1535	19970205 <--
CA 2244891	AA	19970828	CA 1997-2244891	19970205 <--
AU 9727997	A1	19970910	AU 1997-27997	19970205 <--
EP 920440	A2	19990609	EP 1997-922283	19970205 <--

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG
R: CH, DE, FR, GB, IT, LI, SE
PRIORITY APPLN. INFO.: US 1996-11359 19960209
WO 1997-US1535 19970205

AB The present invention describes a method for identifying one or more of a plurality of sequences differing by one or more single base changes, insertions, deletions, or translocations in a plurality of target nucleotide sequences. The method includes a ligation phase, a capture phase, and a detection phase. The ligation phase utilizes a ligation detection reaction between one **oligonucleotide** probe, which has a target sequence-specific portion and an addressable **array** -specific portion, and a second **oligonucleotide** probe, having a target sequence-specific portion and a detectable label. After the ligation phase, the capture phase is carried out by hybridizing the ligated **oligonucleotide** probes to a solid support with an **array** of immobilized capture **oligonucleotides** at least some of which are complementary to the addressable **array** -specific portion. Following completion of the capture phase, a detection phase is carried out to detect the labels of ligated **oligonucleotide** probes hybridized to the solid support. The ligation phase can be preceded by an amplification process. The present invention also relates to a kit for practicing this method, a method of forming **arrays** on solid supports, and the supports themselves.

L14 ANSWER 30 OF 37 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:35735 CAPLUS

DOCUMENT NUMBER: 126:115285
TITLE: Ultrathin **oligonucleotide** layers for fluorescence based **DNA**-sensors
AUTHOR(S): Furch, M.; Ueberfeld, J.; Hartmann, A.; Bock, D.; Seeger, S.
CORPORATE SOURCE: Physikalisch-Chemisches Inst., Univ. Heidelberg, Heidelberg, 69120, Germany
SOURCE: Proc. SPIE-Int. Soc. Opt. Eng. (**1996**), 2928(Biomedical Systems and Technologies), 220-226
CODEN: PSISDG; ISSN: 0277-786X
PUBLISHER: SPIE-The International Society for Optical Engineering
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Preliminary investigations into the design of an affinity sensor using evanescent wave technol. conc. upon the means of immobilization of the receptor mols. In this work **DNA** served as the selective recognition element. The mol. principle of a sequence-selective biosensor for **DNA** is based on a sandwich-hybridization assay wherein the analyte, a single-stranded (ss)**DNA**, bound specifically to both an immobilized capture probe and a dye-labeled **oligonucleotide** in free soln. The efficiency of the capture **array** depends on the d. of highly organized **oligonucleotides** on the waveguide surface and correlates therefore directly with the specificity and the sensitivity of the sensor. In the present approach using the Langmuir-Blodgett technique cinnamoylbutylether-cellulose monolayers were transferred onto optical fibers or planar waveguides. These films served as matrixes for the immobilization of biotinylated **oligonucleotides** via streptavidin. For the first time streptavidin was immobilized by that manner. The specificity of the streptavidin layer or the following bounded **nucleic acid** mols. were controlled by an ELISA. Finally, this application has also shown to be suitable for the detection of Salmonella, which is an important pathogen assocd. with acute gastroenteritidis and **food** borne diseases.